Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-46. (Cancelled)

47. (New) A method for determining a predisposition for a manifestation of an immune system related disease in an individual comprising, determining in a biological sample isolated from said individual the presence or absence of a polymorphism, said polymorphism being located within a fragment of MASP-2 consisting of the CUB1, EGF, CUB2, CCP1 and CCP2 domains and/or located within the amino acid sequence of MAp-19,

wherein said polymorphism is within the amino acid sequence of the MASP-2 protein as identified in SEQ ID NO: 1, or the Map-19 protein as identified in SEQ ID NO: 2, said polymorphism being a substitution, deletion and/or addition of at least one amino acid residue or

wherein said polymorphism is within the coding DNA sequence of human MASP-2 as identified in SEQ ID NO: 3 or the MAp-19 protein as identified in SEQ ID NO: 4, said

polymorphism being a substitution, deletion and/or addition of at least one nucleotide within said coding sequence.

48. (New) The method of claim 47, wherein the polymorphism is a substitution, deletion and/or addition of at least one amino acid located within a fragment of MASP-2 consisting of the CUB1, EGF, CUB2 domains.

49. (New) The method of claim 47, wherein the polymorphism is a substitution, deletion and/or addition of at least one amino acid located within a fragment of MASP-2 consisting of the CUB1 and EGF domains.

50. (New) The method of claim 47, wherein the polymorphism is a substitution, deletion and/or addition of at least one amino acid located within a fragment of MASP-2 and/or MAp-19 consisting of CUB1.

51. (New) The method according to claim 47, wherein the polymorphism is a substitution, deletion and/or addition of at least one amino acid located within the range of amino acid residues from position 80 to position 120 according to the amino acid sequences set forth in SEQ ID NO: 1 or 2.

52. (New) The method according to claim 47, wherein the polymorphism being a substitution for Asp or deletion of Asp in position 105 according to the amino acid sequences set forth in SEQ ID NO: 1 or 2.

53. (New) The method of claim 52, the polymorphism being Asp→Gly.

54. (New) The method according to claim 47, wherein the polymorphism is determined by isolating the MASP-2 and/or MAp-19 proteins from a biological sample collected from an individual and ascertaining the substitution/mutation in the amino acid sequence of said proteins by a method selected from the group consisting of mass-spectroscopy methods, MALDI-TOF mass-spectroscopy, protein sequencing methods and immunoassays.

55. (New) The method according to claim 47 further comprising isolating the MBL-MASP or ficolin-MASP complexes from a biological sample collected from an individual and examining the ability of the complex to activate C4 complement.

56. (New) The method according to claim 47 further comprising examining the protein composition of MBL or ficolin complexes in a biological sample collected from an individual.

57. (New) The method according to claim 47, wherein the predisposition to a manifestation of an immune system related disease is determined by the absence of the MASP-2 (SEQ ID NO: 1) and/or MAp19 (SEQ ID NO: 2) proteins in the MBL or ficolin complexes.

58. (New) The method according to claim 47, wherein the presence or absence of the polymorphism is detected by hybridising a probe to a target nucleic acid sequence comprising at least position 359 according to the SEQ ID NO: 3 or SEQ ID NO: 4 or the corresponding position of the complementary strand.

59. (New) The method of claim 47, the polymorphism being a single nucleotide substitution/mutation A→G in position 359 corresponding to the sequence set forth in SEQ ID NO: 3.

60. (New) The method according to claim 59, wherein the probe is bound to a detectable label.

61. (New) The method according to claim 60, wherein the label is selected from the group consisting of fluorescent reporter groups, enzyme tags, chemiluminescent groups and radioisotopes.

62. (New) The method according to claim 59, comprising the use of a capture probe for capturing a target nucleic acid sequence.

63. (New) The method according to claim 59, comprising amplification of a nucleotide sequence comprising the polymorphism.

64. (New) The method according to claim 63, wherein amplification comprises use of a primer pair comprising SEQ ID NO: 5 and 6, or SEQ ID NO: 7 and 8.

65. (New) The method according to claim 47, wherein the presence or absence of the polymorphism is detected by using isolation of a target nucleic acid from an individual, said target nucleic acid comprising at least position 359 according to the sequence set forth in the SEQ ID NO: 3 or the

corresponding position of the complementary strand, and sequencing of said isolated target nucleic acid.

66. (New) The method according to claim 47, further comprising assessing the alleles at nucleotide no. 359 according to the sequence set forth in SEQ ID NO: 3 in a target nucleotide sequence corresponding to SEQ ID NO: 3 or the complementary strand.

67. (New) An isolated oligonucleotide comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 or the corresponding complementary strand, said isolated oligonucleotide sequence comprising the G allele in position 359 or the corresponding allele of the complementary strand.

68. (New) The isolated oligonucleotide according to claim 67, comprising at least 15 contiguous nucleotides, more preferably at least 20 nucleotides.

69. (New) The isolated oligonucleotide according to claim 67, wherein the oligonucleotide is a polynucleotide sequence encoding the MASP-2 polypeptide having Gly at position 105 according to the amino acid sequence set forth in SEQ ID NO: 1.

70. (New) The isolated oligonucleotide according to claim 67, wherein the oligonucleotide is a polynucleotide sequence encoding the MAp-19 polypeptide having Gly at position 105 according to the amino acid sequence set forth in SEQ ID NO: 2.

71. (New) The isolated oligonucleotide or polynucleotide sequence according to claim 67, wherein the nucleotides are selected from the group consisting of RNA, DNA, LNA, PNA monomers and chemically modified nucleotides capable of hybridising to a target sequence.

72. (New) An isolated antibody capable of recognition of the MASP-2 and/or MAp-19 polypeptides, or a selective binding fragment of such an antibody, wherein

(1) said polypeptides and fragments comprise Gly in position 105 according to the SEQ ID NOS: 1 or 2, and said recognition is by selectively binding to an epitope comprising said Gly, or selectively binding to an epitope created within said polypeptides or said fragments, due to mutation of Asp→Gly in position 105 according to SEQ ID NOS:1 or 2, or

(2) said polypeptides and fragments comprise Asp in position 105 according to the SEQ ID NOS: 1 or 2, and said

recognition is by selectively binding to an epitope comprising said Asp, or selectively binding to an epitope created within said polypeptides or said fragments, due to Asp in position 105 according to SEQ ID NOS:1 or 2.

73. (New) A kit for predicting an increased risk of a subject of developing an immunologic disease comprising

(1) at least one probe comprising a oligonucleotide sequence, said oligonucleotide sequence comprising at least 10 contiguous oligonucleotides of SEQ ID NO: 3 or the corresponding complementary strand, said isolated oligonucleotide sequence comprising the G allele in position 359 or the corresponding allele of the complementary strand and/or

(2) at least one probe comprising at least one antibody, or a selective binding fragment of an antibody, as defined by claim 72.

74. (New) The kit according to claim 73, wherein the probe is linked to a detectable label.

75. (New) The kit according to claim 73, further comprising a set of primers for amplifying a region of the human MASP-2 gene, said region comprising position 359

according to SEQ ID NO: 3 or the corresponding complementary strand.

76. (New) A method of treatment of an individual having a predisposition to a manifestation of an immune system related disease comprising

I) identification of a mutation in the MASP-2 gene of said individual and

II) administering to said individual an effective amount of a polypeptide comprising SEQ ID NO:1 and/or polypeptide comprising SEQ ID NO:2.

77. (New) An isolated polypeptide selected from the group consisting of

(1) an isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 1 or SEQ ID NO 2 or a fragment thereof, said polypeptide or said fragment comprising Gly in position 105 according to said sequence,

(2) an isolated polypeptide, wherein the polypeptide is a peptide fragment having a size in a range from 5 to 160 amino acids derived from the amino acid sequence set forth in SEQ ID NO: 1 comprising at least 5 amino acid contiguous sequence, said sequence corresponding to amino acid residues 100-105, 101-106, 102-107, 103-108, 104-109 and/or 105-110 of

the sequence set forth in SEQ ID NO: 1, wherein Gly in position 105 of said sequence is substituted for Asp, and

(3) an isolated polypeptide, wherein the polypeptide is a peptide fragment having a size in a range from 5 to 160 amino acids derived from the amino acid sequence set forth in SEQ ID NO: 1 comprising at least 5 amino acid contiguous sequence, said sequence corresponding to amino acid residues 100-105, 101-106, 102-107, 103-108, 104-109 and/or 105-110 of the sequence set forth in SEQ ID NO: 1.

78. (New) A gene therapy vector for the treating pathologic conditions associated with high or low activity of MBL-pathway,

said vector comprising the sequence identified as SEQ ID NO: 3, or a fragment thereof, operably linked to a promoter sequence capable of directing the in vivo expression of MASP-2 encoded by SEQ ID NO: 3 or

said vector comprising the nucleotide sequence identified as SEQ ID NO: 3, said sequence having substitution A→G in position 359, said sequence operably linked to a promoter sequence capable of directing the in vivo expression of MASP-2 having glycine residue in position 105 according the sequence set forth in SEQ ID NO: 1.

79. (New) The gene therapy vector according to claim 78, for treating pathologic conditions associated with low activity of MBL-pathway in a subject carrying the G allele in the position corresponding to nucleotide position 359 of the sequence identified in SEQ ID NO: 3.

80. (New) The gene therapy vector according to claim 78 for treating pathologic conditions associated with low activity of MBL-pathway, wherein said vector comprising the sequence identified as SEQ ID NO: 3, or a fragment thereof operably linked to a promoter sequence capable of directing the in vivo expression of MASP-2 encoded by SEQ ID NO: 3.

81. (New) The gene therapy vector of claim 78, for treating therapeutic conditions associated with pathologically high activity of the MBL-pathway, said vector comprising the nucleotide sequence identified as SEQ ID NO: 3, except that said sequence has the substitution A→G in position 359, said sequence operably linked to a promoter sequence capable of directing the in vivo expression of MASP-2 having glycine residue in position 105 according the sequence set forth in SEQ ID NO: 1.

82. (New) A method of treatment for inhibition of activity of the lectin-complement pathway, comprising administering to an individual an effective amount of an agent selected from the group consisting of:

(1) an isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 1 or SEQ ID NO 2 or a fragment thereof, said polypeptide or said fragment comprising Gly in position 105 according to said sequence,

(2) an isolated oligonucleotide comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 or the corresponding complementary strand, said isolated oligonucleotide sequence comprising the G allele in position 359 or the corresponding allele of the complementary strand, and

(3) an isolated antibody capable of recognition of the MASP-2 and MAp-19 polypeptides or fragments thereof by selectively binding to an epitope comprising Asp corresponding to position 105 of the sequence set forth in SEQ ID NOS: 1 or 2.

83. (New) The method according to claim 82, for the inhibition of activity of the lectin-complement pathway, comprising administering a polypeptide sequence as set forth in SEQ ID NOS: 1 or 2, or a fragment thereof, said polypeptide

or said fragment comprising Gly in position 105 of said sequences.

84. (New) The method according to claim 82, for inhibition of activity of the lectin-complement pathway comprising administering, an isolated oligonucleotide comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 or the corresponding complementary strand, said isolated oligonucleotide sequence comprising the G allele in position 359 or the corresponding allele of the complementary strand.

85. (New) The method according to claim 82, for the inhibition of activity of the lectin-complement pathway, comprising administering an isolated antibody capable of recognition of the MASP-2 and MAp-19 polypeptides, or a selective binding fragment thereof, by selectively binding to an epitope comprising Asp corresponding to position 105 of the sequence set forth in SEQ ID NOS: 1 or 2.

86. (New) The method according to claim 82, for treatment of therapeutic conditions associated with pathologically high activity of the lectin-complement pathway.

87. (New) The method according to claim 82, wherein the therapeutic conditions associated with pathologically high activity of MBL-complement pathway being an inflammatory disease, ischemia, apoptosis or atherosclerosis.